REMARKS

Claims 1-13 and 49-56 are pending in the present application. Upon entry of the instant amendments, Claims 1-2, 4-9, 11-13, 50-52, and 54-56 as amended, and new claims 59-88, will be pending.

Claims 1-2, 7-9, 11-12, 50-52, and 54-56 have been amended to better define certain embodiments of the invention, notwithstanding the Applicants' belief that the unamended claims would have been allowable, and without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute in the future the unamended (or similar) claims in another application, for the purpose of furthering the Applicants' business goals and expediting the patent application process in a manner consistent with the PTO's Patent Business Goals (PBG).[1] None of the amendments to the claims is related to the statutory requirements of patentability unless expressly stated so herein. No amendment made herein was intended to narrow the scope of any of the amended claims.

In particular, Claim 1 has been amended to cancel reference to percent sequence identity and algorithm, and to recite a protein "comprising amino acids 1 to 357 of SEQ ID NO:1. " Support for this amendment is in the Specification, page 9, lines 6-12 which teaches this specific domain and its location. Claim 11 has been amended to depend from Claim 1.

Claims 2 and 12 have been amended to provide further clarity to the term "TL- γ" by adding reference to "Thermomyces lanuginosus- " and "SEQ ID NO:1."

Claims 7 and 53-56 have been amended to delete reference to hybridization under stringent conditions. Claim 7 has additionally been amended to recite that the nucleic acid sequence comprises sequence 5' GATATTTCCACCGCCCGACAT 3' and/or sequence 5' TGAAAACAGCGAAGCAGGAATTC 3' which are the complement of SEQ ID NO:3 and 4, respectively. Support for these added sequences is in the originally-filed Claim 7 which recites a sequence that is amplified by, and that hybridizes under stringent conditions to, SEQ ID NOs: 3 or 4, respectively; the newly added sequences satisfy these recitations as they are 100% complementary to the originally-recited SEQ ID NOs: 3 and 4. Claims 54-56 have been further amended to avoid potential duplication of amended Claims 50-52.

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[1] 65 Fed. Reg. 54603 (September 8, 2000).

Claim 8 has been amended by replacing the term "derived" with "isolated" as supported by the Specification, page 11, lines 13-22. The term "fungi" was replaced with "fungus" to correct a grammatical error.

Claim 9 has been amended by adding the term "said fungus" to provide antecedent basis and further clarity.

Claims 50-52 have been amended by adding "sequence" for further clarity, and canceling reference to a sequence which has greater than a particular % sequence identity.

New Claims 61, 64 and 65 recite the specific fragments of SEQ ID NO:1 as supported in the specification (see, for example, page 6, lines 1-4, page 8, lines 13-29, and page 9, lines 1-13). New Claims 62 and 63 additionally recite that the encoded protein has plus-end directed microtubule motor activity, and binds to the specified antibodies, as was supported by original Claims 1 and 2.

New Claims 66-60 additionally recite that the encoded protein further comprises additional amino acid sequence domains of SEQ ID NO:1, and that the encoded protein has plus-end directed microtubule motor activity (Claim 67); support is provided throughout the specification (see, for example, page 8, lines 13-29 and page 9, lines 1-12).

New Claims 71-73 recite the polymorphic variants of TL- γ which have amino acid substitutions in the tail domain as described in the Specification, page 9, lines 15-20.

New Claim 74 is directed to a nucleic acid sequence amplified by the specified primer set (supported is provided, for example, on page 25, lines 12-18, and page 56, lines 22-29), new Claim 75 is recites that the encoded protein has plus end-directed microtubule motor activity (as was provided in original Claim 1), and new Claim76 is directed a nucleic acid sequence amplified by the specified primer set (supported is provided, for example, on page 25, lines 12-15).

New Claims 77, 79, 81 and 83 are directed to expression vectors comprising the specified nucleic acid sequences (supported is provided, for example, on page 15, lines 4-8), and new Claims 78, 80, 82 and 84 are directed to host cells comprising the specified expression vectors (supported is provided, for example, on page 21, lines 7-11).

New Claims 85-88 are directed to isolated nucleic acid sequences which encode protein with the specified properties; support for these claims is found throughout the specification (see,

for example, page 5, lines 21-25 and page 8, lines 16-19 for Claim 85; page 5, lines 26-28 and page 8, lines 20-22 for Claim 86; page 5, lines 29-32 and page 8, lines 23-35 for Claim 87; and page 6, lines 1-4 and page 8, lines 25-29 for Claim 88).

Finally, Claim 3 has been cancelled to avoid potential duplication of amended Claim 2. Claim 6 has been cancelled to avoid potential lack of antecedent basis for the term "algorithm." Claim 10 has been cancelled to avoid potential lack of antecedent basis for the term "hybridizes under stringent hybridization conditions." Claim 53 has been cancelled to avoid potential duplication of amended Claim 49.

In the Office Action dated October 9, 2002, the Examiner made a number of objections and rejections. For clarity, the objections and rejections at issue are set forth by number in the order they are herein addressed:

(1) The Examiner requested that the claim to priority be corrected;

(2) The Examiner requested that the use of the trademark PILEUP™ be capitalized and accompanied by generic terminology;

(3) Claims 1-13 and 49-56 are rejected under 35 USC 112, first paragraph, as allegedly insufficiently described;

(4) Claims 1-13 and 49-56 are rejected under 35 USC 112, first paragraph, as allegedly non-enabled;

(5) Claims 1-13 and 49-56 are rejected under 35 USC 112, second paragraph, as allegedly indefinite;

(6) Claim 6 is rejected under 35 USC 112, second paragraph, as allegedly indefinite;

(7) Claims 7, 10 and 53-56 are rejected under 35 USC 112, second paragraph, as allegedly indefinite; and

(8) Claims 8-9 are rejected under 35 USC 112, second paragraph, as allegedly indefinite.

Applicants believe that the following remarks traverse the Examiner's rejections of the claims. These remarks are presented in the same order as the above objections and rejections.

1. The claim to priority has been amended

The Examiner requested that the claim to priority be corrected, on the basis that the parent application has become abandoned (Office Action, item 3, page 2). In particular, the Examiner requested that the expression "now abandoned" should follow the filing date of the parent application.

The Applicants have amended the specification such that the phrase "now abandoned" follows the filing date of the parent application. Thus, the Applicants' claim to priority has been corrected.

2. Trademarks are capitalized and accompanied by generic terminology

The Examiner has required that the use of the trademark PILEUP™ be capitalized wherever it appears and be accompanied by generic terminology (Office Action, item 4, pages 2-3). The Applicants note that the trademark PILEUP is capitalized in the specification and in the claims, and is accompanied by the generic terminology, such as "a sequence comparison algorithm" (see, for example, Claim 6, and the specification, page 15, line 25 to page 16, line 11). Therefore, the Applicants use of the trademark PILEUP is in accordance with the Examiner's requirement.

3. The claims are sufficiently described.

Claims 1-13 and 49-56 are rejected under 35 USC 112, first paragraph, as allegedly insufficiently described (Office Action, item 5, page 3 to page 10). The Applicants respectfully disagree, for the reasons provided below.

A. Claims 4-5 Should Be Allowed

The Applicants note that the Examiner ADMITS MANY TIMES that SEQ ID NO:2 meets the written description requirement (see, for example, Office Action, page 5, second full paragraph). Claim 5 is directed to an isolated nucleic acid sequence of Claim 1, wherein the nucleic acid has a nucleotide sequence of SEQ ID NO:2; as the Examiner has admitted that SEQ ID NO:2 meets the written description requirement, Claim 5 is sufficiently described. Therefore, for these reasons alone, CLAIM 5 SHOULD BE ALLOWED.

Claim 4 is directed to an isolated nucleic acid sequence of Claim 1, wherein the nucleic acid encodes SEQ ID NO:1. According to the Revised Interim Written Description Guidelines Training Materials (Downloaded from the USTPO website on 10/10/00), one of skill in the art would conclude that the Applicants were in possession of the genus based on the specification and the general knowledge in the art concerning a genetic coding table (Example 11: Allelic Variants). This is based upon the rationale that Claim 4 is drawn to the genus of nucleic acid sequences that encode amino acid sequence SEQ ID NO:1, i.e., all sequences degenerately related by a genetic code table to SEQ ID NO:2. Although one species within the genus is disclosed (in the exemplary specification described in the guidelines; more species are actually disclosed in the Applicants' specification, as described further below), i.e., SEQ ID NO:2, a person of skill in the art could readily envision all the nucleic acids degenerate to SEQ ID NO:2 by using a genetic code table. Based upon the Guidelines, Claim 4 should not be rejected under the written description requirement. Therefore, for these additional reasons, CLAIM 4 SHOULD BE ALLOWED.

Claim 3 has been canceled [2]; therefore, the Examiner's rejection as to this claim is moot.

B. Recitation of Percent Identity: Claim 1

The Examiner asserts that the claims and specification fail to provide the identity or structure of this isolated nucleic acid sequence (Office Action, page 3), that the specification does not provide evidence of a nucleic acid sequence, other than the sequence of SEQ ID NO:2 that can encode a microtubule motor protein (Office Action, page 4), that there is evidence that other sequences have not yet been identified (Office Action, page 4), that the specification and claims describe an isolated nucleic acid by its encoded protein function, but that this description does not describe the claimed nucleic acid itself (Office Action, pages 4-5), that the specification has not defined what the "30-40%" variation can be (Office Action, page 6), that "the specification does not provide any representative examples of isolated nucleic acid sequences having 60-70% identity to SEQ ID NO:2, that there is "no teaching or [sic] which nucleic acids

[2] Claim 3 was canceled, notwithstanding Applicant's belief that Claim 3 would have been allowable, without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute the cancelled (or similar) claim in another application, for the purpose of furthering Applicant's business goals and expediting the patent application process.

may or may not be changed without causing detrimental effects towards the production of a microtubule motor protein which retains the recited properties" (Office Action, page 7), and that the specification lacks examples of species of a genus of nucleic acids (Office Action, page 7). The Examiner concludes that therefore "the full breadth of the claims fails to meet the written description provision of 35 USC 112, first paragraph" (Office Action, page 8).

The Applicants note that these reasons are directed particularly to Claim 1, and NOT TO ALL the claims. Moreover, the Examiner improperly narrows the scope of the claims. Claim 1 is directed to subject matter comprising a nucleic acid sequence encoding a protein, where a property of the protein is **greater than 60%** amino acid sequence identity to a TL-γ tail domain, BUT NOT to subject matter comprising a nucleic acid sequence with **60%-70%** identity to SEQ ID NO:2, as is frequently recited by the Examiner in the reasons directed particularly to Claim 1.

In addition, in contrast to the Examiner's frequent recitation that the specification lacks teaching or examples of isolated nucleic acid sequences having greater than 60% identity to SEQ ID NO:2, the specification on page 9, lines 6-20, describes three polymorphic variants of TL-γ. These variants are described in terms of amino acid substitutions; once these variants are provided, it is a trivial matter to determine nucleic acid sequences that encode these variants, and these nucleic acid sequences have greater than 60% identity to SEQ ID NO:2. Thus, the specification DOES provides representative examples of isolated nucleic acid sequences having 60-70% identity to SEQ ID NO:2, and DOES provide examples of species of the genus of claimed nucleic acids (the isolated nucleic acids of Claim 1). For these reasons, Claim 1 is sufficiently described, and the Applicants respectfully request the withdrawal of this rejection of the claim.

Moreover, the specification also provides teaching of conservatively modified variants of nucleotide and amino acid sequences (see, for example, page 12, line 13 to page 13, line 13); once a polypeptide sequence is determined, it is routine to determine nucleic acid sequences which encode such polypeptide variants (as, for example, by reference to a genetic code table). For these reasons as well, Claim 1 is sufficiently described, and the Applicants respectfully request the withdrawal of this rejection of the claim.

Nonetheless, the Applicants have amended Claims 1 and 11 to recite the specifically-identified motor domain sequence and to cancel recitation to percent sequence identity.[3] Accordingly, this rejection of these claims should be withdrawn.

C. Recitation of primers: Claim 7

The Examiner asserts that the claim and specification lack sufficient written description of the "GENERICALLY CLAIMED PRIMER" (Office Action, page 8; emphasis added). Moreover, the Examiner asserts that there is evidence that other primers have not yet been identified (Office Action, page 8).

However, this improperly narrows the scope of the claims, since Claim 7 is not limited to a primer but rather encompasses an isolated sequence of Claim 1 with the properties claimed in Claim 7. Furthermore, the Applicants HAVE identified other primers; such primers are provided in Example I (see page 56, lines 23-29, SEQ ID NOs: 5-7). Therefore, the Examiner's assertions are WRONG, and the basis of the rejection of Claim 7 unfounded.

Nonetheless, Applicants have amended Claim 7 to cancel reference to hybridization to the primers, and to insert specifically identified sequences that are present in the isolated sequence.[4] As explained above, support for these added sequences is in the originally-filed Claim 7 which recites a sequence that is amplified by, and that hybridizes under stringent conditions to, SEQ ID NOs: 3 or 4, respectively; the newly added sequences satisfy these recitations as they are 100% complementary to the originally-recited SEQ ID NOs: 3 and 4. Thus, for this additional reason, the Applicants believe that Claim 7 is sufficiently described, and respectfully request withdrawal of this rejection of the claim.

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[3] These amendments were made notwithstanding Applicant's belief that the unamended claims would have been allowable, without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute the cancelled (or similar) claim in another application, for the purpose of furthering Applicant's business goals and expediting the patent application process.

[4] These amendments were made notwithstanding Applicant's belief that the unamended claims would have been allowable, without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute the cancelled (or similar) claim in another application, for the purpose of furthering Applicant's business goals and expediting the patent application process.

D. Recitation of Hybridization Conditions: Claim 10

The Examiner asserts that the specification and claims lack sufficient written description of hybridization between an unidentified nucleic acid and a target sequence (SEQ ID NO:2) wherein a 40% mismatch is encountered (Office Action, page 9). However, a 40% mismatch IS NOT RECITED by Claim 10; therefore, this assertion is irrelevant to the subject matter of the claim.

The Examiner further asserts that the claim is directed to a PROBE, when the Examiner asserts that the description of the ability of the "CLAIMED PROBE" (emphasis added) to hybridize to SEQ ID NO:2 may describe the hybridization conditions (Office Action, page 9). In contrast to the Examiner's assertion, the claim is NOT LIMITED to a PROBE, but includes any isolated nucleic acid sequence of Claim 1. Therefore, this assertion is incorrect as well.

Nonetheless, Applicants have cancelled Claim 10 and amended Claims 7 and 53-56 to cancel recitation of hybridization.[5] For these reasons, the Applicants respectfully request the withdrawal of this rejection of the claim.

E. Recitation of Percent Identity

The Applicants note that new Claims 85-89 are directed to subject matter comprising a nucleic acid sequence encoding a protein with greater than 95% sequence identity to specified amino acid sequences, and which has plus end-directed microtubule motor activity. These claims are supported by the specification, as described above; moreover, the Applicants submit that under the analysis provided in the Written Description Guidelines (WDG), these claims are allowable. Thus, as provided in WDG Example 14, a claim to a protein of a specified amino acid sequence and variants that are at least 95% identical to the specified sequence which has a specified activity satisfies the written description requirement, because the Applicants' specification provide the sequence of the protein, SEQ ID NO:1, and also provides three exemplary variants of the protein, which are at least 95% identical to SEQ ID NO:1. Moreover,

[5] These cancellations and amendments were made notwithstanding Applicant's belief that the originally-filed claims would have been allowable, without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute the cancelled (or similar) claim in another application, for the purpose of furthering Applicant's business goals and expediting the patent application process.

the specification describes how to make variants, and provides assays for determining the activity of variants.[6] As provided in WDG Example 11, where an isolated DNA encodes a protein with a specified amino acid sequence, a person of skill in the art could readily envision all the DNAs degenerate to the specified amino acid sequence by using a genetic code table, and by the same means could envision all the DNAs which encode an amino acid sequence with at least 95% identity to the specified amino acid sequences.

4. The claims are enabled.

Claims 1-13 and 49-56 are rejected under 35 USC 112, second paragraph, as allegedly non-enabled (Office Action, item 6, page 10 to page 14). The Applicants respectfully disagree, for the reasons established below.

A. Claims 4 and 5 Should be Allowed

The Applicants note that the Examiner ADMITS SEVERAL TIMES that the specification discloses a nucleic acid sequence encoding a plus-end directed microtubule motor protein having a nucleotide sequence of SEQ ID NO:2 (see, for example, Office Action, page 11, first full paragraph). Since Claim 5 recites these limitations, CLAIM 5 SHOULD BE ALLOWED.

Claim 4 is directed to an isolated nucleic acid sequence of Claim 1, wherein the nucleic acid encodes SEQ ID NO:1. As described above, Claim 4 is drawn to the genus of nucleic acid sequences that encode amino acid sequence SEQ ID NO:1, i.e., all sequences degenerately related by a genetic code table to SEQ ID NO:2. At least three four species of this genus are described in the specification: TL-γ and three variants (see, for example, page 9, line 1-20). One exemplary coding sequence is provided for TL-γ (i.e., SEQ ID NO:2). A person of skill in the art could readily determine nucleic acids encoding the variants by using a genetic code table. Moreover, that same person could readily determine all remaining nucleic acids degenerate to

[6] Thus, the specification provides descriptions of how to synthesize nucleic acid sequences which encode variants (see, for example, page 24, lines 24-30), how to express protein products of such synthesized nucleic acid sequences (see, for example, page 27, line 18 to page 30, line 16 and page 57, line 15 to page 58, line 4), how to purify the expressed protein product (see, for example, page 30, line 18 to page 33, line 4 and page 58, lines 5-18), and how to assay the products for plus end-directed microtubule motor activity (see, for example, page 58, line 20 through page 59, line 29).

SEQ ID NO:2 by using a genetic code table. Therefore, Claim 4 is enabled. For these additional reasons, CLAIM 4 SHOULD BE ALLOWED.

Claim 3 has been canceled [7]; therefore, the Examiner's rejection as to this claim is moot.

B. Determining % Sequence Identity is Routine

The Examiner asserts generally that "[t]he claims are drawn to an isolated nucleic acid sequence encoding a microtubule motor protein, wherein the protein has the following properties: (i) the protein's activity includes plus end-directed microtubule motor activity; and (ii) the protein has a tail domain that has greater than 60% amino acid sequence identity to a TL-gamma tail domain as measured using a sequence comparison algorithm or *a nucleic acid sequence comprising a sequence which has greater than 60% identity with SEQ ID NO:2* (Office Action, item 6, page 11; emphasis added). Although not specifically stated, the Applicants assume that the first part of the description refers to Claim 1, and that the second part of the description (indicated by italics) refers to Claim 49. The Applicants remarks are accordingly premised on the assumption that this rejection is directed particularly to Claims 1 and 49.

The Examiner asserts that "[t]he specification fails to teach the identity of any other nucleic acid sequences with the claimed abilities" (Office Action, item 6, page 11), that the specification is not enabled for any variants of a polynucleotide comprising a sequence having 60% identity to SEQ ID NO:2 (Office Action, item 6, page 11), that "the specification lacks any written description of a structure or relevant identifying characteristics of a representative number of polynucleotides encoding a representative number of proteins sufficient to allow one skilled in the art to determine that **the inventor had possession of the invention as claimed**" (Office Action, item 6, page 11; emphasis added), and that the specification does not provide guidance or working examples to determine nucleic acids with additions, substitutions, and deletions (Office Action, item 6, page 12).

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[7] Claim 3 was canceled, notwithstanding Applicant's belief that Claim 3 would have been allowable, without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute the cancelled (or similar) claim in another application, for the purpose of furthering Applicant's business goals and expediting the patent application process.

With respect to the Examiner's assertion indicating possession of the invention, as indicated by bold text above, this comment is irrelevant because it relates to a written description rejection, and not to an enablement rejection.

The Examiner's other assertions are wrong. There is no requirement that the specification describe actual experiments or examples of all of the nucleic acid sequences claimed. In fact, the legal standard of enablement is satisfied when the specification provides **reasonable guidance** on how to obtain the claimed nucleic acid sequences. The Federal Circuit has enunciated this principle by holding that:

> "[i]t is *not necessary* that a patent applicant *test all the embodiments* of his invention. . . ; what is necessary is that he provide a disclosure sufficient to enable one skilled in the art to carry out the invention commensurate with the scope of his claims."[8] Enablement is satisfied "if the specification in question provides a *reasonable amount of guidance* with respect to the direction in which the experimentation should proceed . . . ."[9]

Reasonable guidance on how to obtain the claimed nucleic acid sequences is provided throughout the specification. Moreover, contrary to the Examiner's assertions, the specification DOES PROVIDE examples of variants of polynucleotides.

In particular, the specification on page 9, lines 15-20, describes three polymorphic variants of TL-γ. These variants are described in terms of amino acid substitutions; once these variants are provided, it is routine to determine nucleic acid sequences which encode these variants, and these coding sequences have greater than 60% identity to SEQ ID NO:2. Thus, the specification DOES provides representative examples of nucleic acid sequences having greater than 60% identity to SEQ ID NO:2, and DOES provide examples of species of the genus of claimed nucleic acids (the isolated nucleic acids of Claim 1). For these reasons, Claims 1 and 49 are enabled, and the Applicants respectfully request the withdrawal of this rejection of these claims.

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[8] (Emphasis added) *Amgen, Inc. v. Chugai Pharmaceutical Co., Ltd.*, 927 F.2d 1200, 18 USPQ2d 1016 (Fed. Cir. 1991).

[9] *Ex parte Jackson,* 217 USPQ 804, 807 (Bd. App. 1982); *In re Wands,* 8 USPQ2d 1400, 1404 (CAFC 1988); see also *Ex parte Forman*, 230 USPQ 546 (BPAI 1986).

Moreover, contrary to what the Examiner apparently believes, it is not necessary to recite what is well known in the art; otherwise, an application becomes unwieldy. "Patent documents are written for persons familiar with the relevant field; the patentee is not required to include in the specification information readily understood by practitioners, lest every patent be required to be written as a comprehensive tutorial and treatise for the generalist, instead of a concise statement for persons in the field" (*Verve v. Crane Cams* (Fed. Cir. Nov 14, 2002).

Thus, the specification also provides teaching of conservatively modified variants of an amino acid sequence (see, for example, page 12, line13 to page 13, line 13); once such variants are determined, it is routine to determine sequences which encode such variants (such as by using a genetic code table). It is also routine to synthesize nucleic acid sequences which encode such variants, as is also described by the specification (see, for example, page 24, lines 24-30), to express protein products of such synthesized nucleic acid sequences (see, for example, page 27, line 18 to page 30, line 16; and page 57, line 15 to page 58, line 4), to purify the expressed protein product (see, for example, page 30, line 18 to page 33, line 4; and page 58, lines 5-18), and to assay the products for plus end-directed microtubule motor activity (see, for example, page 58, line 20 through page 59, line 29). Thus, contrary to the Examiner's assertions, the specification DOES provide teaching of nucleic acid sequences encoding variants of a microtubule motor protein (such as TL-γ) that retain the recited properties.

The specification also provides teaching of how to obtain sequences which have greater than 60% sequence identity with SEQ ID NO:2 (see, for example, descriptions of how to obtain sequences which encode TL-γ on page 25, line 5 to page 27, line 16; descriptions of how to determine sequences of a particular identity, page 15, line 13 to page 17, line 11; and descriptions of how to determine sequences which can hybridize to SEQ ID NO:2 under stringent conditions, page 17, line 24 to page 18, line 14).

For these reasons as well, Claims 1 and 49 are enabled, and the Applicants respectfully request the withdrawal of this rejection of these claims.

Finally, the Examiner asserts that random altering of nucleic acids would lead to unpredictable results regarding the cross reactivity of the isolated bacterium (Office Action, item 6, page 12). Since the claims do not recite reactivity of isolated bacterium, this assertion is irrelevant to the rejection of the claims based on enablement.

Nonetheless, the Applicants' amendment of Claims 1, 8, 9, 11, and 50-52 to cancel recitation of sequence identity, and the Applicants' cancellation of Claim 49, moots this rejection.[10] Therefore, this rejection of the claims should be withdrawn.

C. Determining Primer Sequence is Routine

The Examiner ADMITS that the specification teaches that primers identified as SEQ ID NO:3 and 4 can be used in amplification techniques (Office Action, item 6, page 13). However, the Examiner asserts that there is no teaching of any other primers being used with hybridization techniques (Office Action, item 6, page 13), and that the "specification appears to make the conclusion that only the primers of SEQ ID NO:3 and 4 will perform in the hybridization experiments" (Office Action, item 6, page 13). The Examiner concludes that the specification fails to enable other generically claimed primers (Office Action, item 6, page 13).

The Applicants note that the specification DOES teach additional primers to amplify a sequence which encodes TL-γ. Moreover, as noted above, the specification provides guidance in obtaining additional sequences which hybridize to a known sequence under stringent conditions (see, for example, page 17, line 24 to page 18, line 14). For these reasons, Claim 7 is enabled, and the Applicants respectfully request the withdrawal of this rejection of this claim.

Nonetheless, Applicants' amendment of Claim 7 to cancel recitation of hybridization to primers, and to add a recitation of the sequence contained in the isolated sequence moots this rejection.[11]

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[10] These amendments and cancellation were made notwithstanding Applicant's belief that the originally-filed claims would have been allowable, without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute the cancelled (or similar) claim in another application, for the purpose of furthering Applicant's business goals and expediting the patent application process.

[11] These amendments were made notwithstanding Applicant's belief that the originally-filed claims would have been allowable, without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute the cancelled (or similar) claim in another application, for the purpose of furthering Applicant's business goals and expediting the patent application process.

4. The claims are definite

Several sets of claims are rejected under 35 USC 112, second paragraph, as allegedly indefinite; the Applicants respectfully disagree with each set of rejections, which are discussed below.

A. "TL-γ " in Claims 1-13 and 49-56

The Examiner asserts that these claims fail to particularly point out and distinctly claim the subject matter which the Applicants regard as the invention, on the ground that acronyms like TL-γ must be spelled out when used for the first time in a chain of claims (Office Action, item 7, page 14).

The Applicants point out first that the term "TL-γ" DOES NOT APPEAR in Claims 49-56; therefore, they respectfully request that the rejection of these claims on this ground be withdrawn.

The Applicants next point that term "TL- γ" is described and defined in several locations within the specification (see, for example, page 7, line 31 to page 8, line 12; and page 23, lines 10-19), and embodiments are also provided (see, for example, page 9, lines 1-12). According to the MPEP Sec. 608.01(o), Basis for Claim Terminology in Description, the meaning of every term used in any of the claims should be apparent from the descriptive portions of the specification with clear disclosure as to its import, and a term used in the claims may be given a special meaning in the description. The meaning of the term "TL- γ" is clear from the specification, and refers to *Thermomyces lanuginosus* gamma protein. Moreover, it is well known that a patentee may be his or her own lexicographer; thus, an applicant is free to use a new term, as long as the term is described in the specification. The Applicants are free to use the term "TL- γ," as it is properly described in the specification. Finally, the Examiner has not cited to any authority for the proposition that acronyms like TL- γ must be spelled out when used for the first time in a chain of claims. Because the term "TL- γ" is described in the specification, and an applicant may be his or her own lexicographer, and because there is no cited authority to the contrary, the Applicants submit that their use of the term "TL- γ" is definite.

Nonetheless, to expedite prosecution and to further the Applicants' business goals, Claims 1 and 11 have been amended to include the phrase "*Thermomyces lanuginosus* gamma"

before the phrase "TL- γ," in accordance with the Examiner's request. Thus, the rejection of Claims 1-13 as indefinite on this ground should be withdrawn.

B. Trademark in Claim 6

The Examiner asserts that the scope of this claim is uncertain due to the presence in the claim of the trademark PILEUP (Office Action, item 8, first part, pages 14-15).

However, this rejection is moot in view of cancellation of Claim 6.[12]

C. Hybridization under "stringent hybridization conditions"

The Examiner asserts that the term "stringent condition" renders claims 7, 10 and 53-56 indefinite, on the ground that the term is not defined by the claims and the specification does not provide a standard for ascertaining the requisite degree (Office Action, item 9, page 15).

In contrast to the Examiner's assertion, the phrase "selectively hybridize" IS DEFINED IN THE SPECIFICATION, as for example, on page 17, line 24 to page 18, line 14, where the definition provides a standard for ascertaining the requisite degree (for example, the specification provides that selective hybridization occurs only to a particular nucleotide sequence under stringent hybridization conditions, and provides exemplary stringent hybridization conditions as including 50% formamide, 5x SSC and 1% SDS, incubating at 42 degrees, or 5x SSC, 1% SDS, incubating at 65 degrees C, with a wash in 0.2x SSC and 0.1% SDS at 65 degrees C).

Thus, contrary to the Examiner's assertion, the definitions provided in the specification DO apprise one of skill of the scope of the invention, and therefore, the claims are definite.

Nonetheless, the Applicants have cancelled claim 10, and amended Claims 7 and 53-56 to delete reference to hybridization under stringent conditions.[13] Accordingly, the rejection should be withdrawn.

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[12] This cancellation was made notwithstanding Applicant's belief that the cancelled claim would have been allowable, without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute the cancelled (or similar) claim in another application, for the purpose of furthering Applicant's business goals and expediting the patent application process.

[13] These amendments and cancellation were made notwithstanding Applicant's belief that the unamended and cancelled claims would have been allowable, without acquiescing to any of the Examiner's arguments, and without waiving the right to prosecute the cancelled (or similar) claim in

D. The term "derived from"

The Examiner asserts that the phrase "TL-γ derived from" is recited in Claims 8-9, but that it is unclear how to define "derived from" (Office Action, page 15, para 10). The Examination further asserts that the specification does not teach how to make derivatives from the recited fungus.

In contrast to the Examiner's interpretation of the phrase "derived from" to mean a "make a derivative from," the Applicants have used the phrase "derived from" to mean obtained from, such that the source of the TL- γ of the claims is a hyphal fungi (Claim 8) or a *Thermomyces lanuginosus* (Claim 9). In fact, the first definition of "derive" in the dictionary (which also includes "derived") is "to take, received or **obtain** esp. **from a specified source**" (Merriam Webster's Collegiate Dictionary, Tenth Edition, 1997; page 311, emphasis added. Copy attached at Tab 1). Moreover, none of the definitions provided in the dictionary are directed to "make a derivative from."

For these reasons, the Applicants submit that the phrase "TL- γ derived from" in Claims 8-9 IS clear, and they respectfully request that the rejection of these claims as indefinite on this ground be withdrawn.

Nonetheless, the Applicants have amended Claim 8 by replacing "derived" with the term "isolated" which is defined in the specification on page 11, lines 13-22. Accordingly, the rejection should be withdrawn.

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another application, for the purpose of furthering Applicant's business goals and expediting the patent application process.

CONCLUSION

For the reasons set forth above, it is respectfully submitted that the Applicants' claims should be allowed. Should the Examiner believe that a telephone interview would aid in the prosecution of this application, the Applicants encourage the Examiner to call the Dr. Maha Hamdan at (415) 904-6500 **before beginning to draft another written communication** (if any).

Dated: 3/10/03

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APPENDIX I

MARKED-UP VERSION OF REWRITTEN, ADDED, AND/OR CANCELLED PARAGRAPHS AND CLAIMS

The following includes a marked-up version of the paragraphs and/or claims pursuant to 37 C.F.R. §§ 1.121 (b)(1)(iii) and 1.121 (c)(1)(ii) with instructions and markings showing changes made herein to the previous version of record of the claims. Brackets denote deleted text, and underlining denotes added text.

IN THE SPECIFICATION:

This is a Divisional Application of Application Serial No. 09/235,416, filed January 23, 1999, which claims benefit under 35 U.S.C. §119(e) to Provisional Patent Application Serial No. 60/072,361 filed on January 23, 1998, now abandoned, which is herein incorporated by reference in its entirety for all purposes.

IN THE CLAIMS:

1. (Amended once) An isolated nucleic acid sequence encoding a [microtubule motor] protein comprising amino acids 1 to 357 of SEQ ID NO:1[, wherein the protein has the following properties:

(i) the protein's activity includes plus end-directed microtubule motor activity; and

(ii) the protein has a tail domain that has greater than 60% amino acid sequence identity to a TL-γ tail domain as measured using a sequence comparison algorithm].

2. (Amended once) [An] The isolated nucleic acid sequence of Claim 1, wherein the protein specifically binds to polyclonal antibodies to *Thermomyces lanuginosus* gamma (TL-γ) protein listed as SEQ ID NO:1.

7. (Once Amended) [An] The isolated nucleic acid sequence of Claim 1 [, wherein the nucleic acid is amplified by primers that selectively hybridize under stringent hybridization conditions to the same sequence as the primer set:] comprising sequence 5' GATATTTCCACCGCCCGACAT 3' that is complementary to 5' ATGTCGGGCGGTGGAAATATC 3' (SEQ ID NO:3), or comprising sequence 5' TGAAAACAGCGAAGCAGGAATTC 3' that is complementary to 5' GAATTCCTGCTTCGCTGTTTTCA 3' (SEQ ID NO:4), wherein said isolated nucleic acid sequence encodes a protein having plus end-directed microtubule motor activity.

8. (Amended once) [An] The isolated nucleic acid sequence of Claim 1, wherein the nucleic acid [has identity to a TL-γ derived] is isolated from a hyphal [fungi] fungus.

9. (Amended once) [An] The isolated nucleic acid sequence of Claim 8, wherein [the nucleic acid has identity to a TL-γ derived from] said fungus is *Thermomyces lanuginosus*.

11. (Amended Once) An expression vector comprising [a] the nucleic acid sequence of Claim 1 [encoding a microtubule motor protein wherein the protein has the following properties:

(i) the protein's activity includes plus end-directed microtubule motor activity; and

(ii) the protein has a tail domain that has greater than 60% amino acid sequence identity to a (TL-γ) tail domain, as measured using a sequence comparison algorithm].

12. (Amended once) [A] The expression vector of Claim 11, wherein the protein specifically binds to polyclonal antibodies to *Thermomyces lanuginosus* (TL- γ) protein listed as SEQ ID NO:1.

50. (Amended once) An isolated nucleic acid sequence comprising [a sequence which has greater than 70% sequence identity with] nucleotides 1-1071 of SEQ ID NO:2.

51. (Amended once) An isolated nucleic acid sequence comprising [a sequence which has greater than 60% sequence identity with] nucleotides 1327-1803 of SEQ ID NO:2.

52. (Amended once) An isolated nucleic acid sequence comprising [a sequence which has greater than 60% sequence identity with] nucleotides 1804-2352 of SEQ ID NO:2.

54. (Amended once) [An isolated nucleic acid sequence which hybridizes under stringent conditions to a complement of nucleotides 1-1071 of SEQ ID NO:2] The nucleotide sequence of Claim 50, wherein said sequence encodes a protein having plus-end directed microtubule motor activity.

55. (Amended once) [An isolated nucleic acid sequence which hybridizes under stringent conditions to a complement of nucleotides 1327-1803 of SEQ ID NO:2] The nucleotide sequence of Claim 51, wherein said sequence encodes a protein having plus-end directed microtubule motor activity.

56. (Amended once) [An isolated nucleic acid sequence which hybridizes under stringent conditions to a complement of nucleotides 1804-2352 of SEQ ID NO:2] The nucleotide sequence of Claim 52, wherein said sequence encodes a protein having plus-end directed microtubule motor activity.

APPENDIX II

CLEAN VERSION OF THE ENTIRE SET OF PENDING CLAIMS AS AMENDED IN THIS COMMUNICATION

The following is a list of the claims as they would appear following entry of this amendment.

1. (Amended once) An isolated nucleic acid sequence encoding a protein comprising amino acids 1 to 357 of SEQ ID NO:1.

2. (Amended once) The isolated nucleic acid sequence of Claim 1, wherein the protein specifically binds to polyclonal antibodies to *Thermomyces lanuginosus* gamma (TL-γ) protein listed as SEQ ID NO:1.

4. An isolated nucleic acid sequence of Claim 1, wherein the nucleic acid encodes SEQ ID NO:1.

5. An isolated nucleic acid sequence of Claim 1, wherein the nucleic acid has a nucleotide sequence of SEQ ID NO:2.

7. (Once Amended) The isolated nucleic acid sequence of Claim 1 comprising sequence 5' GATATTTCCACCGCCCGACAT 3' that is complementary to 5' ATGTCGGGCGGTGGAAATATC 3' (SEQ ID NO:3), or comprising sequence 5' TGAAAACAGCGAAGCAGGAATTC 3' that is complementary to 5' GAATTCCTGCTTCGCTGTTTTCA 3' (SEQ ID NO:4), wherein said isolated nucleic acid sequence encodes a protein having plus end-directed microtubule motor activity.

8. (Amended once) The isolated nucleic acid sequence of Claim 1, wherein the nucleic acid is isolated from a hyphal fungus.

9. (Amended once) The isolated nucleic acid sequence of Claim 8, wherein said fungus is *Thermomyces lanuginosus*.

11. (Amended Once) An expression vector comprising the nucleic acid sequence of Claim 1.

12. (Amended once) The expression vector of Claim 11, wherein the protein specifically binds to polyclonal antibodies to *Thermomyces lanuginosus* (TL- γ) protein listed as SEQ ID NO:1.

13. A host cell transfected with the vector of Claim 11.

50. (Amended once) An isolated nucleic acid sequence comprising nucleotides 1-1071 of SEQ ID NO:2.

51. (Amended once) An isolated nucleic acid sequence comprising nucleotides 1327-1803 of SEQ ID NO:2.

52. (Amended once) An isolated nucleic acid sequence comprising nucleotides 1804-2352 of SEQ ID NO:2.

54. (Amended once) The nucleotide sequence of Claim 50, wherein said sequence encodes a protein having plus-end directed microtubule motor activity.

55. (Amended once) The nucleotide sequence of Claim 51, wherein said sequence encodes a protein having plus-end directed microtubule motor activity.

56. (Amended once) The nucleotide sequence of Claim 52, wherein said sequence encodes a protein having plus-end directed microtubule motor activity.

59. The nucleic acid sequence of Claim 1, wherein the protein has plus end-directed microtubule motor activity.

60. The nucleic acid sequence of Claim 11, wherein the protein has plus end-directed microtubule motor activity.

61. An isolated nucleic acid sequence encoding a protein comprising amino acids 602 to 784 of SEQ ID NO:1.

62. The nucleic acid sequence of Claim 61, wherein the protein has plus end-directed microtubule motor activity.

63. The isolated nucleic acid sequence of Claim 62, wherein the protein specifically binds to polyclonal antibodies to *Thermomyces lanuginosus* gamma (TL-γ) protein listed as SEQ ID NO:1.

64. An isolated nucleic acid sequence encoding a protein comprising amino acids 358 to 442 of SEQ ID NO:1.

65. An isolated nucleic acid sequence encoding a protein comprising amino acids 443-601 of SEQ ID NO:1.

66. The isolated nucleic acid sequence of Claim 1, wherein the encoded protein further comprises amino acids 602 to 784 of SEQ ID NO:1.

67. The nucleic acid sequence of Claim 66, wherein the protein has plus end-directed microtubule motor activity

68. The isolated nucleic acid sequence of Claim 1, wherein the encoded protein further comprises amino acids 358 to 442 of SEQ ID NO:1.

69. The isolated nucleic acid sequence of Claim 1, wherein the encoded protein further comprises amino acids 443 to 601 of SEQ ID NO:1.

70. The isolated nucleic acid of Claim 1, wherein the encoded protein further comprises at least one of amino acids 602 to 784 of SEQ ID NO:1, amino acids 358 to 442 of SEQ ID NO:1, and amino acids 443 to 601 of SEQ ID NO:1.

71. An isolated nucleic acid sequence encoding a protein comprising a variant of amino acids 602 to 784 of SEQ ID NO:1, wherein the variant comprises isoleucine substituted for valine at amino acid position 713.

72. An isolated nucleic acid sequence encoding a protein comprising a variant of amino acids 602 to 784 of SEQ ID NO:1, wherein the variant comprises glutamic acid substituted for aspartic acid at amino acid position 762.

73. An isolated nucleic acid sequence encoding a protein comprising a variant of amino acids 602 to 784 of SEQ ID NO:1, wherein the variant comprises aspartic acid substituted for glutamic acid at amino acid position 774.

74. The isolated nucleic acid sequence of Claim 1, wherein the nucleic acid is amplified by primer set SEQ ID NO:5 and SEQ ID NO:6 or by primer set SEQ ID NO:5 and SEQ ID NO:7.

75. The nucleic acid sequence of Claim 74, wherein the protein has plus end-directed microtubule motor activity.

76. The isolated nucleic acid sequence of Claim 1, wherein the nucleic acid is amplified by the primer set:

5' ATGTCGGGCGGTGGAAATATC 3' (SEQ ID NO:3)

5' GAATTCCTGCTTCGCTGTTTTCA 3' (SEQ ID NO:4)

77. An expression vector comprising the nucleic acid sequence of Claim 4.

78. A host cell transfected with the vector of Claim 77.

79. An expression vector comprising the nucleic acid sequence of Claim 63.

80. A host cell transfected with the vector of Claim 79.

81. An expression vector comprising the nucleic acid sequence of Claim 64.

82. A host cell transfected with the vector of Claim 81.

83. An expression vector comprising the nucleic acid of Claim 60.

84. A host cell transfected with the vector of Claim 83.

85. An isolated nucleic acid sequence encoding a microtubule motor protein, wherein the protein has the following properties:

(i) the protein has greater than 95% amino acid sequence identity to SEQ ID NO:1 as measured using a sequence comparison algorithm; and

(ii) the protein has plus end-directed microtubule motor activity.

86. An isolated nucleic acid sequence encoding a microtubule motor protein, wherein the protein has the following properties:

(i) the protein has a domain that has greater than 95% amino acid sequence identity to amino acids 1 to 357 of SEQ ID NO:1 as measured using a sequence comparison algorithm; and

(ii) the protein plus end-directed microtubule motor activity.

87. An isolated nucleic acid sequence encoding a microtubule motor protein, wherein the protein has the following properties:

(i) the protein has a domain that has greater than 95% amino acid sequence identity to amino acids 443-601 of SEQ ID NO:1 as measured using a sequence comparison algorithm; and

(ii) the protein has plus end-directed microtubule motor activity.

88. An isolated nucleic acid sequence encoding a microtubule motor protein, wherein the protein has the following properties:

(i) the protein has a domain that has greater than 95% amino acid sequence identity to amino acids 601 to 784 of SEQ ID NO:1 as measured using a sequence comparison algorithm; and

(ii) the protein has plus end-directed microtubule motor activity.